

Team 5

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/447,118

CRF Processing Date: 8/5/95
Edited by: MB
Verified by: MB (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- ☒ Edited a format error in the Current Application Data section, specifically:

See bottom PSL

ENTERED

- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____

- ☐ Added the mandatory heading and subheadings for "Current Application Data".

- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- ☐ Inserted colons after headings/subheadings. Headings edited included:

- ☐ Deleted extra, invalid, headings used by an applicant, specifically:

- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____

- ☐ Inserted mandatory headings, specifically: _____

- ☐ Corrected an obvious error in the response, specifically:

- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

- ☐ Corrected an error in the Number of Sequences field, specifically:

- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- ☐ Other: _____

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/447,118DATE: 08/10/95
TIME: 08:26:52

INPUT SET: S5462.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT:

(A) NAME: Burkly, Linda C.
(B) STREET: 34 Winthrop Street
(C) CITY: West Newton
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 02165

(A) NAME: Biogen, Inc.
(B) STREET: Fourteen Cambridge Center
(C) CITY: Cambridge
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 02142

(ii) TITLE OF INVENTION: TREATMENT FOR INSULIN DEPENDENT DIABETES

(iii) NUMBER OF SEQUENCES: 15

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 000000 (BGP-151CP) ← add (B) Filing date:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US94/01456
(B) FILING DATE: 09-FEB-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/029,330
(B) FILING DATE: 09-FEB-1993

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/447,118DATE: 08/10/95
TIME: 08:26:57

INPUT SET: S5462.raw

47
48 (ii) MOLECULE TYPE: cDNA
49
50
51 (ix) FEATURE:
52 (A) NAME/KEY: CDS
53 (B) LOCATION: 1..360
54
55 (ix) FEATURE:
56 (A) NAME/KEY: misc_feature
57 (B) LOCATION: 1
58 (D) OTHER INFORMATION:/note= "pBAG159 insert: HP1/2 heavy
59 chain variable region; amino acid 1 is Glu (E) but
60 Gln(Q) may be substituted"
61
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
63
64 GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA 48
65 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
66 1 5 10 15
67
68 GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT 96
69 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
70 20 25 30
71
72 ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA 144
73 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
74 35 40 45
75
76 AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG 192
77 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
78 50 55 60
79
80 GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG 240
81 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
82 65 70 75 80
83
84 CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA 288
85 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
86 85 90 95
87
88 GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA 336
89 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
90 100 105 110
91
92 GGG ACC ACG GTC ACC GTC TCC TCA 360
93 Gly Thr Thr Val Thr Val Ser Ser
94 115 120
95
96
97 (2) INFORMATION FOR SEQ ID NO: 2:
98
99 (i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/447,118DATE: 08/10/95
TIME: 08:27:02

INPUT SET: S5462.raw

100 (A) LENGTH: 120 amino acids
101 (B) TYPE: amino acid
102 (D) TOPOLOGY: linear
103
104 (ii) MOLECULE TYPE: protein
105 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
106
107 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
108 1 5 10 15
109
110 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
111 20 25 30
112
113 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
114 35 40 45
115
116 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
117 50 55 60
118
119 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
120 65 70 75 80
121
122 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
123 85 90 95
124
125 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
126 100 105 110
127
128 Gly Thr Thr Val Thr Val Ser Ser
129 115 120
130
131 (2) INFORMATION FOR SEQ ID NO: 3:
132
133 (i) SEQUENCE CHARACTERISTICS:
134 (A) LENGTH: 318 base pairs
135 (B) TYPE: nucleic acid
136 (C) STRANDEDNESS: single
137 (D) TOPOLOGY: linear
138
139 (ii) MOLECULE TYPE: cDNA
140
141
142 (ix) FEATURE:
143 (A) NAME/KEY: CDS
144 (B) LOCATION: 1..318
145 (D) OTHER INFORMATION:/product= "HP1/2 light
146 chain variable region"
147
148 (ix) FEATURE:
149 (A) NAME/KEY: misc_feature
150 (B) LOCATION: 1
151 (D) OTHER INFORMATION:/note= "pBAG172 insert: HP1/2 light
152 chain variable region"

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/447,118DATE: 08/10/95
TIME: 08:27:08

INPUT SET: S5462.raw

153
154
155 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
156
157 AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA 48
158 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
159 125 130 135
160
161 GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT 96
162 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
163 140 145 150
164
165 GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA 144
166 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
167 155 160 165
168
169 TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC 192
170 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
171 170 175 180
172
173 AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT 240
174 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
175 185 190 195 200
176
177 GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC 288
178 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
179 205 210 215
180
181 ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC 318
182 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
183 220 225
184
185
186 (2) INFORMATION FOR SEQ ID NO: 4:
187
188 (i) SEQUENCE CHARACTERISTICS:
189 (A) LENGTH: 106 amino acids
190 (B) TYPE: amino acid
191 (D) TOPOLOGY: linear
192
193 (ii) MOLECULE TYPE: protein
194 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
195
196 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
197 1 5 10 15
198
199 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
200 20 25 30
201
202 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
203 35 40 45
204
205 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly

RAW SEQUENCE LISTING PATENT APPLICATION US/08/447,118

DATE: 08/10/95
TIME: 08:27:13

INPUT SET: S5462.raw

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206          50          55          60
207
208 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
209 65          70          75          80
210
211 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
212          85          90          95
213
214 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
215          100          105
216

```

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..429

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..57

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 58..429

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "pBAG195 insert: AS heavy chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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248
249 ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT          48
250 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
251 -19          -15          -10          -5
252
253 GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA          96
254 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
255          1          5          10
256
257 CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GCG TCT GGC TTC AAC ATT          144
258 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile

```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/447,118DATE: 08/10/95
TIME: 08:27:18**INPUT SET: S5462.raw**

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Burkly, Linda C.
7	Unknown or Misplaced Identifier	(B) STREET: 34 Winthrop Street
8	Unknown or Misplaced Identifier	(C) CITY: West Newton
9	Unknown or Misplaced Identifier	(D) STATE: Massachusetts
10	Unknown or Misplaced Identifier	(E) COUNTRY: USA
11	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 02165
13	Unknown or Misplaced Identifier	(A) NAME: Biogen, Inc.
14	Unknown or Misplaced Identifier	(B) STREET: Fourteen Cambridge Center
15	Unknown or Misplaced Identifier	(C) CITY: Cambridge
16	Unknown or Misplaced Identifier	(D) STATE: Massachusetts
17	Unknown or Misplaced Identifier	(E) COUNTRY: USA
18	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 02142

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/08/447,118

DATE: 08/10/95
TIME: 08:27:20

INPUT SET: S5462.raw

ADDRESSEE
STREET
CITY
STATE
COUNTRY
ZIP
CORRESPONDENCE ADDRESS
APPLICATION NUMBER
FILING DATE
CLASSIFICATION

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/447,118DATE: 08/15/95
TIME: 10:51:37

INPUT SET: S5462.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT:

(A) NAME: Burkly, Linda C.
(B) STREET: 34 Winthrop Street
(C) CITY: West Newton
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 02165

(A) NAME: Biogen, Inc.
(B) STREET: Fourteen Cambridge Center
(C) CITY: Cambridge
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 02142

(ii) TITLE OF INVENTION: TREATMENT FOR INSULIN DEPENDENT DIABETES

(iii) NUMBER OF SEQUENCES: 15

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US94/01456
(B) FILING DATE: 09-FEB-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/029,330
(B) FILING DATE: 09-FEB-1993

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid

RAW SEQUENCE LISTING PATENT APPLICATION US/08/447,118

 DATE: 08/15/95
 TIME: 10:51:42

INPUT SET: S5462.raw

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47         (C) STRANDEDNESS: single
48         (D) TOPOLOGY: linear
49
50     (ii) MOLECULE TYPE: cDNA
51
52
53     (ix) FEATURE:
54         (A) NAME/KEY: CDS
55         (B) LOCATION: 1..360
56
57     (ix) FEATURE:
58         (A) NAME/KEY: misc_feature
59         (B) LOCATION: 1
60         (D) OTHER INFORMATION:/note= "pBAG159 insert: HP1/2 heavy
61             chain variable region; amino acid 1 is Glu (E) but
62             Gln(Q) may be substituted"
63
64     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
65
66     GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA      48
67     Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
68         1             5             10             15
69
70     GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT      96
71     Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
72             20             25             30
73
74     ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA      144
75     Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
76             35             40             45
77
78     AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG      192
79     Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
80             50             55             60
81
82     GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG      240
83     Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
84             65             70             75             80
85
86     CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA      288
87     Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
88             85             90             95
89
90     GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA      336
91     Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
92             100             105             110
93
94     GGG ACC ACG GTC ACC GTC TCC TCA      360
95     Gly Thr Thr Val Thr Val Ser Ser
96             115             120
97
98
99     (2) INFORMATION FOR SEQ ID NO: 2:
  
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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/447,118DATE: 08/15/95
TIME: 10:51:47

INPUT SET: S5462.raw

100

101

(i) SEQUENCE CHARACTERISTICS:

102

(A) LENGTH: 120 amino acids

103

(B) TYPE: amino acid

104

(D) TOPOLOGY: linear

105

106

(ii) MOLECULE TYPE: protein

107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

108

109 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser

110

1 5 10 15

111

112 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr

113

20 25 30

114

115 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly

116

35 40 45

117

118 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln

119

50 55 60

120

121 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu

122

65 70 75 80

123

124 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala

125

85 90 95

126

127 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln

128

100 105 110

129

130 Gly Thr Thr Val Thr Val Ser Ser

131

115 120

132

133 (2) INFORMATION FOR SEQ ID NO: 3:

134

135 (i) SEQUENCE CHARACTERISTICS:

136

(A) LENGTH: 318 base pairs

137

(B) TYPE: nucleic acid

138

(C) STRANDEDNESS: single

139

(D) TOPOLOGY: linear

140

141

(ii) MOLECULE TYPE: cDNA

142

143

144 (ix) FEATURE:

145

(A) NAME/KEY: CDS

146

(B) LOCATION: 1..318

147

(D) OTHER INFORMATION:/product= "HP1/2 light
chain variable region"

148

149

150 (ix) FEATURE:

151

(A) NAME/KEY: misc_feature

152

(B) LOCATION: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/447,118DATE: 08/15/95
TIME: 10:51:52

INPUT SET: S5462.raw

(D) OTHER INFORMATION:/note= "pBAG172 insert: HP1/2 light
chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

153	AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA	48
154	Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly	
155		
156		
157		
158		
159		
160		
161	125 130 135	
162		
163	GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT	96
164	Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp	
165	140 145 150	
166		
167	GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA	144
168	Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile	
169	155 160 165	
170		
171	TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC	192
172	Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly	
173	170 175 180	
174		
175	AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT	240
176	Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala	
177	185 190 195 200	
178		
179	GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC	288
180	Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr	
181	205 210 215	
182		
183	ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC	318
184	Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile	
185	220 225	
186		
187		

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

198	Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly	
199	1 5 10 15	
200		
201	Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp	
202	20 25 30	
203		
204	Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile	
205	35 40 45	

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/447,118DATE: 08/15/95
TIME: 10:51:57

INPUT SET: S5462.raw

206
207 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
208 50 55 60
209
210 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
211 65 70 75 80
212
213 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
214 85 90 95
215
216 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
217 100 105
218

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..429

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..57

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 58..429

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "pBAG195 insert: AS heavy chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

250
251 ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT 48
252 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
253 -19 -15 -10 -5
254
255 GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA 96
256 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
257 1 5 10
258

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/447,118DATE: 08/15/95
TIME: 10:52:02**INPUT SET: S5462.raw**

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Burkly, Linda C.
7	Unknown or Misplaced Identifier	(B) STREET: 34 Winthrop Street
8	Unknown or Misplaced Identifier	(C) CITY: West Newton
9	Unknown or Misplaced Identifier	(D) STATE: Massachusetts
10	Unknown or Misplaced Identifier	(E) COUNTRY: USA
11	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 02165
13	Unknown or Misplaced Identifier	(A) NAME: Biogen, Inc.
14	Unknown or Misplaced Identifier	(B) STREET: Fourteen Cambridge Center
15	Unknown or Misplaced Identifier	(C) CITY: Cambridge
16	Unknown or Misplaced Identifier	(D) STATE: Massachusetts
17	Unknown or Misplaced Identifier	(E) COUNTRY: USA
18	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 02142